

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
 CCCGCCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTTCGCCTTGCTGACGGCGTCTG
 AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
 GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA
 CCCTTCTGTGGGGCTCAATTTTGGAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
 CTCCTTCAAGTGGTTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
 GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC
 CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCT
 TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAA
 GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTGCCAGGCTGGAG
 TGCAGTGGCAGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG
 ATGTACGTGACGACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
 GAACGTGTACGCGCCGGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC
 CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC
 GAGAAAGTGGTGCTGGTGTCTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGA
 CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
 AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCCGCCAGTCCGCG
 GGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTCTCTCCATCGGGC
 CATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
 CCAAGAAGGTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCA
 GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
 TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
 CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT
 ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
 AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGGAAGCTCAAGGAGAAGAAGATGGC
 TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
 TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
 TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC
 TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
 ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT
 CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTCGACCCAGACTGCCACTGC
 CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGCTCAACCTTGTTCTGTCTGT
 TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTGGTAGTTTGGGA
 TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAGTCTATACACAGGGGTGG
 TCTCTTCAATAAAGAAGTGTTGATTAGAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

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FGTGLFGSKPATGFTTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGW\$LALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVIYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLEFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVS NKMRFQLNLFQRDPEEIIWSMSPVVDGVVIPDD
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMM
IVQDATFVYATLQTAHYHRETMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCTCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
AGTCAGTGATGGTGCCGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA
CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGAAGTGAACAAC
CAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC
GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAGTGTCTCCTTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTCACAGTACTTCTTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT
CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCAGGACC
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTATCAGCATTTTACGTGACAACAC
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT
TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCGAG
AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
GGTGAAGGCTGGGGATTTCAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCAGC
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA
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AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCCTCGGGTT
CAAGTGGAGCACGAAGGAGAGTTTACCTGCCACGCTCGGCACCCACTGGGCTCCAGCACGT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGCTGGCCCTGATCATCATGAAG
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CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCTGTAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGGGAGTTTCGAGACCAGCCTG
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
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CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCGG
TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA
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GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT
TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAA